

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Barnwell, John
- (ii) TITLE OF INVENTION: Plasmodium vivax Blood Stage Antigens,
Monoclonal Antibodies, and Diagnostic Assays
- (iii) NUMBER OF SEQUENCES: 2
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Darby and Darby
 - (B) STREET: 805 Third Ave.
 - (C) CITY: New York
 - (D) STATE: New York
 - (E) COUNTRY: USA
 - (F) ZIP: 10022-7513
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER: US
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Gogoris, Adda
 - (B) REGISTRATION NUMBER: 29,714
 - (C) REFERENCE/DOCKET NUMBER: 5986/07686
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: (212)527-7700
 - (B) TELEFAX: (212)753-6237
 - (C) TELEX: 236687

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3337 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Plasmodium vivax

(vii) IMMEDIATE SOURCE:

(B) CLONE: PvMB3.3.1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAATTCGGT AAAGTAACAA CTATGTTTC GTATCTATAT ATAACCTTAC TAATTTTATC 60
TTTTGCTTTT CTTTAAATTC ATGCTTCAAC AGTAAGATAA AAATAATCTA TAAAAACTGC 120
TATATATACA TATATATTCA TAAGTGGCAT TTGTGAATTG CGATCATTTA AATTACGTA 180
AAAACAATAT TGAAAAAAT TTTTTTTTTT TTTTTTTTTT TGTCTACAG AACGATTTAG 240
AATTGGAAAA TGCTTCTGAT GATGTTGTAG AGGTGGAGGA TCCTTCAAAC GACGGTTTAG 300
AATTAGAAGA GGAAATTTT GATGAGAATT CAGGTGATGA TGAACTCTT TTAGATGCTA 360
CCCCGAAGA TGAATTTGCC TTAACAGATT TGCCAATTGA AGACGATGAG GAAGTCAACG 420
AAACGTTAGA TGGAGGTGAA TCATTAGGAG AGGTTTCCAC TGAAGATATG GAAACAGAAG 480
ATGGCTCAAC AGATGATACG GAAACAGAAG AAGGACTACC TGGTGATATG GAAGGAGAAG 540
AAGAAGCTGG CGATATGGAA GCAGGGGAAG AAGCTGGTGA TTTGGAAGCA GGGGAAGAAA 600
CTGGCGATTT GGAAGCAGGG GAAGAACTG GCGATTTGGA AGCAGGGGAA GAAGCTGGTG 660
ATTTGGAAGC AGGGGAAGAA ACTGGCGATT TGGAAGCAGG GGAAGAACT GGAGATGCGG 720
AAACTGAAGA AGGAGCAACT GGAGATGCGG AACTGAAAA TGGAGCAACT GTGTATGTAG 780
ACACAGAAGA TAGTTCAGCT GATGGAGCAG AAAAAGTACA TCTTCCTGCT CAAGAAAATG 840
TACAACCTGC CGATAGTAAT GATGCCCTCT TTGGAAGTAT TTTGGATAAA GATATAATTT 900
TTGATCATAT TAAAGATTTT GAGCCACTAT TCGAACAAAT TGTGGCGGGT ACTGCTAAAC 960
ATGTTACGGG ACAAGAATTG CCAATGAAAC CTGTACCATT ACCAGTGGCA GAAGAGCCCC 1020
CGCAAGTACC AGCGGAAGAA TTAGATGCCA CTCCAGAGGA TGAATTCGCA TTAGATGTTA 1080
CAGAATCTCC CGAGGAAGTA GAATTAGTAT TAGATGAAGA GGCAACTGAA GAAGAATCAA 1140
CGGAAGTGGG ACCAACGGAA GAAGGACCAA CCGAAGAATT AGATGCCACT CCAGAGGATG 1200
GATTTGCGAT TAGACGAAAC TGCAGAAGGA GAAACAGAAG AAACGTAGAG GGAGAAGAAA 1260
CAGAAGAAGC TGCAGAAGGA GAAGTATCAG AAGAACTCC AGAAGGAGAA GAAGAGTTAG 1320

AGGCAACTCC	AGAGGATGAT	TTCGCATTAG	ATGGAACTAC	ATTAGAAGAA	ACCGAAGAAA	1380
CTGCAGAAGG	AGAAGAAACC	GTAGAGGGAG	AAGAAACCGT	AGAGGGAGAA	GAAACCGTAG	1440
AGGGAGAAGA	AGCTGCAGAA	GGAGAAGAAG	AGTTAGAGGC	AACTCCAGAG	GATGACTTCC	1500
AATTAGAAGA	ACCATCAGGA	GAAGGAGAAG	GGGAAGGAGA	AGGAGAAGGG	GAAGGAGAAG	1560
GAGAAGCGTT	AGTAGCAGTG	CCAGTAGTGG	CCGAACCGGT	AGAAGTAGTG	ACTCCTGCTC	1620
AGCCTGTCAA	ACCAATGGTC	GCTCCAACGG	CAGATGAAAC	TTTATTCGTT	GATATCTTAG	1680
ATAACGATTT	AACGTATGCA	GACATTACAT	CCTTTGAGCC	ATTATTTAAA	CAAATCCTCA	1740
AGGATCCTGA	TGCAGGAGAG	GCTGTAACAG	TACCATCAAA	GGAAGCACCT	GTACAAGTAC	1800
CAGTGGCAGT	AGGGCCCGCG	CAAGAAGTGC	CAACGGAAGA	ATTGATGCAA	CTCCAAGAGG	1860
ACGATTTCGA	ATTAGAAGGA	ACTGCAGAAG	CTCCAGAGGA	AGGAGAATTA	GTATTAGAAG	1920
GAGAAGGAGA	ACCAACGGAA	GAAGAGCCAA	GAGAAGGAGA	GCCAACAGAA	GGAGAAGTGC	1980
CAGAGAAGA	ATTAGAGGCA	ACTCCAGAGG	ACGATTTCGA	ATTAGAAGAA	CCAACAGGAG	2040
AAGAAGTAGA	AGAAACCGTA	GAGGGCGAAG	AAACTGCAGA	AGGAGAAGAA	GTGGAAGAGG	2100
TACCTGCAGA	AGTAGAAGAA	GTGGAAGAGG	TACCTGCAGA	AGTAGAAGAA	GTGGAAGAGG	2160
TACCAGAAGA	AGTAGAAGAG	GTACCCGCAG	AAGTAGAAGA	AGTGGAAGAG	GTACCAGAAG	2220
AAGTGGAAGA	GGTACCAGAA	GAAGTGGAAG	AGGTACCAGA	AGAAGTGGA	GAGGTACCAG	2280
AAGAAGTGA	AGAAGTGGA	GAAGTAGAAG	AAGTAGAGGT	ACCAGCGGTA	GTAGAAGTAG	2340
AAGTACCAGC	GGTAGTAGAA	GAAGAGGTGC	CAGAAGAAGT	AGAAGAAGAA	GAAGAAGAGG	2400
AAGAACCACT	AGAGGAAGAA	GATGTATTAC	AATTAGTAAT	ACCATCGGAA	GAAGATATAC	2460
AATTAGACAA	ACCAAAGAAA	GACGAATTAG	GCTCTGGAAT	TTTATCTATC	ATCGACATGC	2520
ACTACCAAGA	CGTTCCAAAG	GAATTTATGG	AAGAAGAAGA	AGAAACTGCA	GTGTATCCAT	2580
TGAAACCAGA	AGATTTTGCA	AAGGAAGATT	CACAATCTAC	AGAATGGCTC	ACATTCATTC	2640
AAGGCCTAGA	AGGCGACTGG	GAACGATTAG	AAGTGAGCTT	AAATAAGGCT	AGAGAAAGAT	2700
GGATGGAACA	AAGAAATAAA	GAATGGGCTG	GCTGGCTTCG	CTTAATTGAA	AATAAATGGT	2760
CAGAATATAG	TCAAATTTCA	ACAAAAGGAA	AGGACCCAGC	TGGTTTGAGA	AAACGAGAGT	2820
GGAGCGACGA	GAAATGGAAA	AAATGGTTTA	AAGCAGAAGT	CAAATCCCAA	ATTGATTCAC	2880
ACTTGAAAAA	ATGGATGAAC	GACACTCATT	CCAATTTATT	TAAAATTCTT	GTGAAAGATA	2940

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TGTCAACAATT TGAAAACAAG AAAACCAAAG AATGGTTAAT GAATCACTGG AAAAAGAACG 3000
 AACGGGGTTA TGGTTCTGAA TCATTGGAAG TTATGACCAC ATCAAAATTA TTAAATGTGG 3060
 CTAAGAGTCG AGAATGGTAC CGTGCCAATC CTAATATAAA TAGAGAAAGA AGAGAACTCA 3120
 TGAAATGGTT TCTCCTAAAA GAAAACGAAT ATTTAGGACA AAGAATGGAA AAAATGGACT 3180
 CATTGGAAAA AAGTTAAATT TTTGTGTTC AATTCAATGT GTACAACATT TTCTGGAAAA 3240
 CGCCTAACCA AGGAAGAATG GAATCAATTT GTTAATGAAA TAAAAGTTTG AATTATAGAA 3300
 AAAAGAACAG ATTATTCTCT TATAAAATTA ATAATTC 3337

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1018 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: C-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Plasmodium vivax

(vii) IMMEDIATE SOURCE:

- (B) CLONE: PvMB3.3.1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Asn Ser Gly Lys Val Thr Thr Met Val Ser Tyr Leu Tyr Ile Thr Leu
 1 5 10 15

Leu Ile Leu Ser Phe Ala Phe Leu Leu Ile His Ala Ser Thr Asn Asp
 20 25 30

Leu Glu Leu Glu Asn Ala Ser Asp Asp Val Val Glu Val Glu Asp Pro
 35 40 45

Ser Asn Asp Gly Leu Glu Leu Glu Glu Glu Asn Phe Asp Glu Asn Ser
 50 55 60

Gly Asp Asp Glu Thr Leu Leu Asp Ala Thr Pro Glu Asp Asp Phe Ala
 65 70 75 80

Leu Thr Asp Leu Pro Ile Glu Asp Asp Glu Glu Val Asn Glu Thr Leu

85

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Asp Gly Gly Glu Ser Leu Gly Glu Val Ser Thr Glu Asp Met Glu Thr
 100 105 110
 Glu Asp Gly Ser Thr Asp Asp Thr Glu Thr Glu Glu Gly Leu Pro Gly
 115 120 125
 Asp Met Glu Gly Glu Glu Glu Ala Gly Asp Met Glu Ala Gly Glu Glu
 130 135 140
 Ala Gly Asp Leu Glu Ala Gly Glu Glu Thr Gly Asp Leu Glu Ala Gly
 145 150 155 160
 Glu Glu Thr Gly Asp Leu Glu Ala Gly Glu Glu Ala Gly Asp Leu Glu
 165 170 175
 Ala Gly Glu Glu Thr Gly Asp Leu Glu Ala Gly Glu Glu Thr Gly Asp
 180 185 190
 Ala Glu Thr Glu Glu Gly Ala Thr Gly Asp Ala Glu Thr Glu Asn Gly
 195 200 205
 Ala Thr Val Tyr Val Asp Thr Glu Asp Ser Ser Ala Asp Gly Ala Glu
 210 215 220
 Lys Val His Val Pro Ala Gln Glu Asn Val Gln Pro Ala Asp Ser Asn
 225 230 235 240
 Asp Ala Leu Phe Gly Ser Ile Leu Asp Lys Asp Ile Ile Phe Asp His
 245 250 255
 Ile Lys Asp Phe Glu Pro Leu Phe Glu Gln Ile Val Ala Gly Thr Ala
 260 265 270
 Lys His Val Thr Gly Gln Glu Leu Pro Met Lys Pro Val Pro Leu Pro
 275 280 285
 Val Ala Glu Glu Pro Ala Gln Val Pro Ala Glu Glu Leu Asp Ala Thr
 290 295 300
 Pro Glu Asp Asp Phe Ala Leu Asp Val Thr Glu Ser Pro Glu Glu Val
 305 310 315 320
 Glu Leu Val Leu Asp Glu Glu Ala Thr Glu Glu Glu Ser Thr Glu Val
 325 330 335
 Gly Pro Thr Glu Glu Gly Pro Thr Glu Glu Leu Asp Ala Thr Pro Glu
 340 345 350
 Asp Gly Phe Arg Ile Arg Arg Asn Cys Arg Arg Arg Asn Arg Arg Asn
 355 360 365
 Val Glu Gly Glu Glu Thr Glu Glu Ala Ala Glu Gly Glu Val Ser Glu

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Glu Thr Pro Glu Gly Glu Glu Glu Leu Glu Ala Thr Pro Glu Asp Asp
385 390 395 400

Phe Ala Leu Asp Gly Thr Thr Leu Glu Glu Thr Glu Glu Thr Ala Glu
405 410 415

Gly Glu Glu Thr Val Glu Gly Glu Glu Thr Val Glu Gly Glu Glu Thr
420 425 430

Val Glu Gly Glu Glu Ala Ala Glu Gly Glu Glu Glu Leu Glu Ala Thr
435 440 445

Pro Glu Asp Asp Phe Gln Leu Glu Glu Pro Ser Gly Glu Gly Glu Gly
450 455 460

Glu Gly Glu Gly Glu Gly Glu Gly Glu Gly Glu Ala Leu Val Ala Val
465 470 475 480

Pro Val Val Ala Glu Pro Val Glu Val Val Thr Pro Ala Gln Pro Val
485 490 495

Lys Pro Met Val Ala Pro Thr Ala Asp Glu Thr Leu Phe Val Asp Ile
500 505 510

Leu Asp Asn Asp Leu Thr Tyr Ala Asp Ile Thr Ser Phe Glu Pro Leu
515 520 525

Phe Lys Gln Ile Leu Lys Asp Pro Asp Ala Gly Glu Ala Val Thr Val
530 535 540

Pro Ser Lys Glu Ala Pro Val Gln Val Pro Val Ala Val Gly Pro Ala
545 550 555 560

Gln Glu Val Pro Thr Glu Glu Leu Met Gln Leu Gln Glu Asp Asp Phe
565 570 575

Glu Leu Glu Gly Thr Ala Glu Ala Pro Glu Glu Gly Glu Leu Val Leu
580 585 590

Glu Gly Glu Gly Glu Pro Thr Glu Glu Glu Pro Arg Glu Gly Glu Pro
595 600 605

Thr Glu Gly Glu Val Pro Glu Glu Glu Leu Glu Ala Thr Pro Glu Asp
610 615 620

Asp Phe Glu Leu Glu Glu Pro Thr Gly Glu Glu Val Glu Glu Thr Val
625 630 635 640

Glu Gly Glu Glu Thr Ala Glu Gly Glu Glu Val Glu Glu Val Pro Ala
645 650 655

Glu Val Glu Glu Val Glu Glu Val Pro Ala Glu Val Glu Glu Val Glu

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Glu Val Pro Glu Glu Val Glu Glu Val Pro Ala Glu Val Glu Glu Val
675 680 685

Glu Glu Val Pro Glu Glu Val Glu Glu Val Pro Glu Glu Val Glu Glu
690 695 700

Val Pro Glu Glu Val Glu Glu Val Pro Glu Glu Val Glu Glu Val Glu
705 710 715 720

Glu Val Glu Glu Val Glu Val Pro Ala Val Val Glu Val Glu Val Pro
725 730 735

Ala Val Val Glu Glu Glu Val Pro Glu Glu Val Glu Glu Glu Glu
740 745 750

Glu Glu Glu Pro Val Glu Glu Glu Asp Val Leu Gln Leu Val Ile Pro
755 760 765

Ser Glu Glu Asp Ile Gln Leu Asp Lys Pro Lys Lys Asp Glu Leu Gly
770 775 780

Ser Gly Ile Leu Ser Ile Ile Asp Met His Tyr Gln Asp Val Pro Lys
785 790 795 800

Glu Phe Met Glu Glu Glu Glu Thr Ala Val Tyr Pro Leu Lys Pro
805 810 815

Glu Asp Phe Ala Lys Glu Asp Ser Gln Ser Thr Glu Trp Leu Thr Phe
820 825 830

Ile Gln Gly Leu Glu Gly Asp Trp Glu Arg Leu Glu Val Ser Leu Asn
835 840 845

Lys Ala Arg Glu Arg Trp Met Glu Gln Arg Asn Lys Glu Trp Ala Gly
850 855 860

Trp Leu Arg Leu Ile Glu Asn Lys Trp Ser Glu Tyr Ser Gln Ile Ser
865 870 875 880

Thr Lys Gly Lys Asp Pro Ala Gly Leu Arg Lys Arg Glu Trp Ser Asp
885 890 895

Glu Lys Trp Lys Lys Trp Phe Lys Ala Glu Val Lys Ser Gln Ile Asp
900 905 910

Ser His Leu Lys Lys Trp Met Asn Asp Thr His Ser Asn Leu Phe Lys
915 920 925

Ile Leu Val Lys Asp Met Ser Gln Phe Glu Asn Lys Lys Thr Lys Glu
930 935 940

Trp Leu Met Asn His Trp Lys Lys Asn Glu Arg Gly Tyr Gly Ser Glu

945

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960

Ser Phe Glu Val Met Thr Thr Ser Lys Leu Leu Asn Val Ala Lys Ser
965 970 975

Arg Glu Trp Tyr Arg Ala Asn Pro Asn Ile Asn Arg Glu Arg Arg Glu
980 985 990

Leu Met Lys Trp Phe Leu Leu Lys Glu Asn Glu Tyr Leu Gly Gln Arg
995 1000 1005

Met Glu Lys Met Asp Ser Leu Glu Lys Ser
1010 1015

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